



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 12:49 pm GMT

PDB ID : 3OGS  
Title : Complex structure of beta-galactosidase from *Trichoderma reesei* with IPTG  
Authors : Maksimainen, M.; Rouvinen, J.  
Deposited on : 2010-08-17  
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

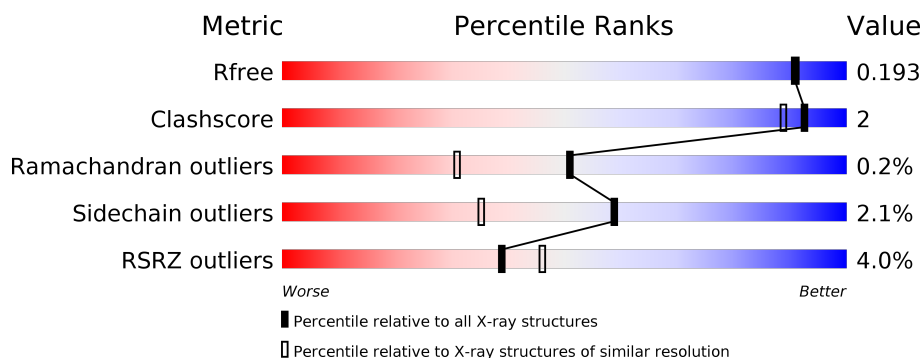
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1762 (1.76-1.76)
Clashscore	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)
RSRZ outliers	101464	1770 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1003	<div> <div>4%</div> <div>87%</div> <div>11%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	A	1038	-	-	-	X
5	NAG	A	1041	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	A	1042	-	-	-	X

## 2 Entry composition [i](#)

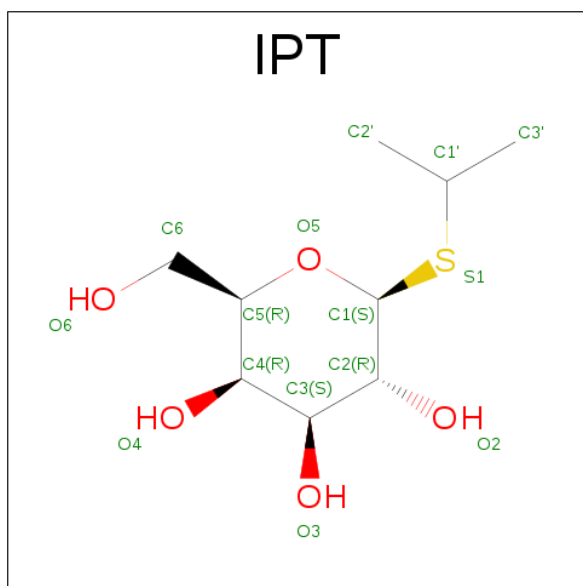
There are 7 unique types of molecules in this entry. The entry contains 8819 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	986	Total	C	N	O	S	0	3	0
			7634	4906	1289	1431	8			

- Molecule 2 is ISOPROPYL-1-BETA-D-THIOGALACTOSIDE (three-letter code: IPT) (formula: C<sub>9</sub>H<sub>18</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			15	9	5	1		

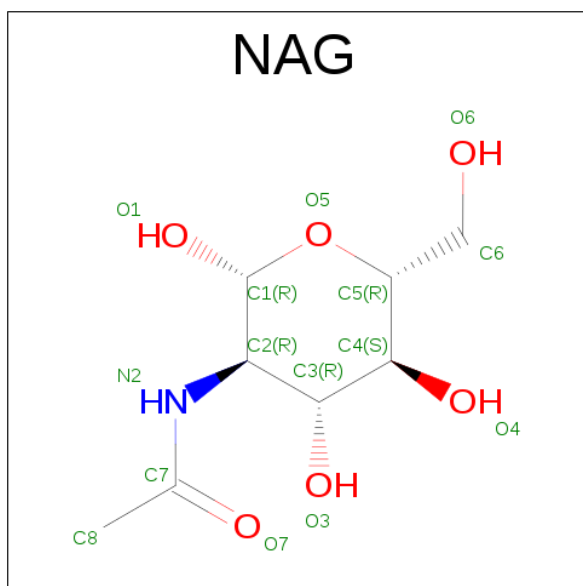
- Molecule 3 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 4 is a polymer of unknown type called SUGAR (9-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	9	Total	C	N	O	0	0
			105	58	2	45		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	2	Total	C	N	O	0	0
			28	16	2	10		

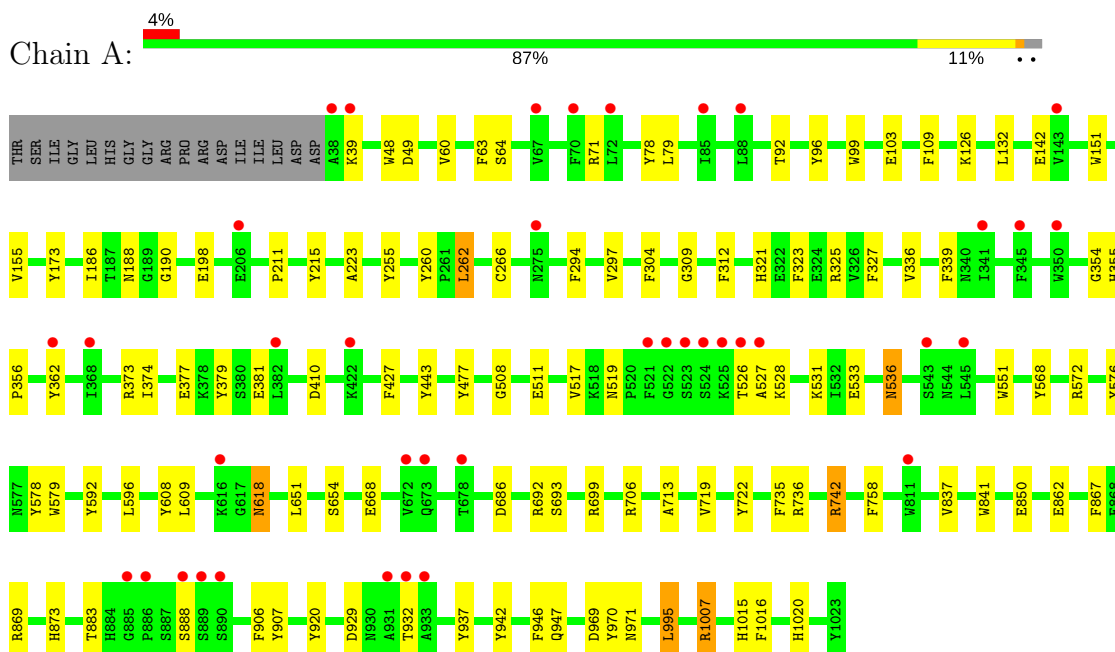
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	926	Total	O	0	0
			926	926		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Beta-galactosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.50Å 70.30Å 82.40Å 108.50° 97.80° 114.40°	Depositor
Resolution (Å)	43.54 – 1.75 43.54 – 1.75	Depositor EDS
% Data completeness (in resolution range)	95.0 (43.54-1.75) 77.3 (43.54-1.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.145 , 0.200 0.159 , 0.193	Depositor DCC
$R_{free}$ test set	5893 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.2	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 64.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for k,h,-h-k-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8819	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, BMA, NAG, IPT, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.78	85/7862 (1.1%)	0.99	18/10715 (0.2%)

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	TYR	CD1-CE1	8.49	1.52	1.39
1	A	937	TYR	CD1-CE1	8.14	1.51	1.39
1	A	109	PHE	CE2-CZ	7.80	1.52	1.37
1	A	103	GLU	CB-CG	7.63	1.66	1.52
1	A	362	TYR	CE2-CZ	7.43	1.48	1.38

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	869	ARG	NE-CZ-NH1	9.01	124.80	120.30
1	A	869	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	A	49	ASP	CB-CG-OD1	8.34	125.81	118.30
1	A	572	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	A	373	ARG	NE-CZ-NH1	6.36	123.48	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7634	0	7435	26	0
2	A	15	0	18	0	0
3	A	83	0	70	0	0
4	A	105	0	88	2	0
5	A	28	0	26	0	0
6	A	28	0	25	0	0
7	A	926	0	0	15	0
All	All	8819	0	7662	28	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 28 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1020:HIS:HB2	7:A:1807:HOH:O	1.20	1.34
1:A:188:ASN:HB3	7:A:1881:HOH:O	1.48	1.14
1:A:531:LYS:HB3	7:A:1575:HOH:O	1.62	0.97
1:A:971:ASN:HB3	7:A:1816:HOH:O	1.67	0.95
4:A:1040:GLC:H61	7:A:1952:HOH:O	1.79	0.82

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	987/1003 (98%)	957 (97%)	28 (3%)	2 (0%)	51 31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	527	ALA

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Mol	Chain	Res	Type
1	A	519	ASN

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	808/819 (99%)	791 (98%)	17 (2%)	59 35

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	536	ASN
1	A	618	ASN
1	A	947	GLN
1	A	528	LYS
1	A	995	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	618	ASN
1	A	1015	HIS
1	A	873	HIS
1	A	412	GLN
1	A	836	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

18 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	NAG	A	1025	1,3	14,14,15	1.25	1 (7%)	15,19,21	1.86	3 (20%)
3	NAG	A	1026	3	14,14,15	1.04	0	15,19,21	0.91	0
3	BMA	A	1027	3	11,11,12	1.58	2 (18%)	13,15,17	1.26	2 (15%)
3	MAN	A	1028	3	11,11,12	1.65	2 (18%)	13,15,17	1.60	2 (15%)
3	MAN	A	1029	3	11,11,12	1.29	2 (18%)	13,15,17	1.63	4 (30%)
3	MAN	A	1030	3	11,11,12	0.67	0	13,15,17	1.56	4 (30%)
3	MAN	A	1031	3	11,11,12	1.30	2 (18%)	13,15,17	2.08	4 (30%)
4	NAG	A	1032	1,4	14,14,15	1.83	2 (14%)	15,19,21	1.69	4 (26%)
4	NAG	A	1033	4	14,14,15	0.78	0	15,19,21	1.41	2 (13%)
4	BMA	A	1034	4	11,11,12	1.08	0	13,15,17	1.48	2 (15%)
4	MAN	A	1035	4	11,11,12	0.88	0	13,15,17	1.53	1 (7%)
4	MAN	A	1036	4	11,11,12	0.63	0	13,15,17	0.99	0
4	MAN	A	1037	4	11,11,12	1.26	1 (9%)	13,15,17	2.51	5 (38%)
4	MAN	A	1038	4	11,11,12	0.96	0	13,15,17	1.84	4 (30%)
4	MAN	A	1039	4	11,11,12	0.96	1 (9%)	13,15,17	2.44	5 (38%)
4	GLC	A	1040	4	11,11,12	0.69	0	13,15,17	2.78	3 (23%)
6	NAG	A	1043	1,6	14,14,15	0.56	0	15,19,21	1.37	3 (20%)
6	NAG	A	1044	6	14,14,15	0.62	0	15,19,21	1.27	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1025	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1026	3	-	0/6/23/26	0/1/1/1
3	BMA	A	1027	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	A	1028	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1029	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1030	3	-	0/2/19/22	0/1/1/1
3	MAN	A	1031	3	-	0/2/19/22	0/1/1/1
4	NAG	A	1032	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1033	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1034	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1035	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1036	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1037	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1038	4	-	0/2/19/22	0/1/1/1
4	MAN	A	1039	4	-	0/2/19/22	0/1/1/1
4	GLC	A	1040	4	-	0/2/19/22	0/1/1/1
6	NAG	A	1043	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	1044	6	-	0/6/23/26	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1031	MAN	O5-C1	-2.45	1.39	1.43
3	A	1025	NAG	C2-N2	2.02	1.49	1.46
3	A	1029	MAN	C2-C3	2.32	1.55	1.52
3	A	1028	MAN	C6-C5	2.36	1.60	1.51
3	A	1029	MAN	O2-C2	2.48	1.48	1.43

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1037	MAN	C6-C5-C4	-6.91	96.82	113.00
4	A	1039	MAN	O3-C3-C4	-4.51	100.55	110.36
3	A	1025	NAG	O5-C1-C2	-3.94	105.99	111.47
4	A	1039	MAN	O2-C2-C1	-3.85	101.34	109.18
4	A	1032	NAG	O5-C1-C2	-3.47	106.65	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1040	GLC	2	0

## 5.6 Ligand geometry

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	IPT	A	1024	-	15,15,15	1.28	1 (6%)	19,21,21	1.57	5 (26%)
5	NAG	A	1041	1	14,14,15	0.56	0	15,19,21	2.45	3 (20%)
5	NAG	A	1042	1	14,14,15	0.53	0	15,19,21	1.83	5 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IPT	A	1024	-	-	0/6/26/26	0/1/1/1
5	NAG	A	1041	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1042	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1024	IPT	C4-C5	3.09	1.59	1.53

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1041	NAG	C1-C2-N2	-3.16	105.09	110.49
5	A	1042	NAG	O3-C3-C2	-3.10	102.75	109.39
5	A	1042	NAG	O7-C7-C8	-3.03	116.55	122.06
2	A	1024	IPT	O2-C2-C3	-2.68	104.54	110.36
2	A	1024	IPT	O4-C4-C3	-2.29	105.37	110.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	986/1003 (98%)	0.01	39 (3%)	39 46	10, 17, 33, 64	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	933	ALA	8.3
1	A	526	THR	7.6
1	A	525	LYS	6.5
1	A	932	THR	6.5
1	A	931	ALA	5.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	MAN	A	1038	11/12	0.94	0.14	3.02	17,22,26,27	0
3	MAN	A	1031	11/12	0.95	0.08	1.08	24,26,28,30	0
6	NAG	A	1043	14/15	0.93	0.14	0.69	32,37,44,46	0
4	NAG	A	1032	14/15	0.93	0.11	0.07	13,18,24,30	0
3	NAG	A	1025	14/15	0.97	0.08	-0.48	13,15,25,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MAN	A	1029	11/12	0.97	0.07	-0.70	15,16,28,35	0
3	NAG	A	1026	14/15	0.97	0.06	-1.27	13,15,21,22	0
4	MAN	A	1039	11/12	0.92	0.12	-	24,30,35,38	0
4	MAN	A	1036	11/12	0.68	0.38	-	55,62,64,65	0
6	NAG	A	1044	14/15	0.76	0.33	-	46,56,63,63	0
3	BMA	A	1027	11/12	0.97	0.07	-	13,16,19,19	0
4	MAN	A	1037	11/12	0.93	0.12	-	22,25,31,34	0
4	GLC	A	1040	11/12	0.80	0.16	-	41,47,48,49	0
3	MAN	A	1028	11/12	0.95	0.08	-	13,15,18,25	0
3	MAN	A	1030	11/12	0.89	0.29	-	30,35,41,47	0
4	BMA	A	1034	11/12	0.97	0.10	-	19,21,25,29	0
4	NAG	A	1033	14/15	0.96	0.13	-	16,23,37,39	0
4	MAN	A	1035	11/12	0.89	0.21	-	34,40,45,48	0

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	1042	14/15	0.93	0.24	6.15	33,39,48,52	0
5	NAG	A	1041	14/15	0.77	0.22	3.18	39,48,56,59	0
2	IPT	A	1024	15/15	0.97	0.11	-0.06	9,12,26,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.